

Sample Submission Guidelines

1. To submit samples for Mass Spectrometry Service, a service request form has to be filled out in FULL, including the sample volume, amount, and concentration. An incomplete request form will be returned and the samples will not be processed.
2. To submit samples for MALDI-TOF analysis, the supervisor's signature is required in the MALDI-TOF sample submission form if 10 samples (or more) are submitted at once.
3. To submit samples for tims-TOF Pro analysis, send the tims-TOF Pro sample submission form via email and copy the email (CC) to your supervisor as a proof of permission.
4. For samples that required protein digestion,
 - i. It is highly recommended to submit 10–100 µg samples to minimize sample loss during processing.
 - ii. Samples should be placed in 1.5mL Eppendorf tubes. Do NOT use 2mL tubes.
 - iii. Sample submitted will be processed by the automated PreON system with the iST kit. The details related to the PreON system can be found at <https://www.preomics.com/preon>.
 - iv. Gel samples are no longer accepted. Please follow the protocol [here](#) to perform in-gel digestion and protein extraction before sample submission.
5. Biohazard and radioactive samples are NOT accepted.
6. At non-office hours, please submit the samples to the 4°C/ -20 °C refrigerator right next to the front door of Room 6127.
7. To minimize human keratin contamination, always wear clean gloves and long-sleeved lab coats.
8. Minimize polymer contamination by
 - i. Using high-quality consumables (e.g., tubes, tips) which have low polymer leaching.
 - ii. Unless necessary, avoid using autoclaved consumables (e.g., tubes, tips).
9. For samples submitted for direct MALDI-MS analysis,
 - i. Minimize salt and additive concentration in samples.
 - ii. Avoid the use of detergents.
 - iii. Desalt using ZipTip™ or Pierce™ C18 Spin Tips may be necessary.
10. The service is on a first-come-first-serve policy. Complete the entire MS Request Form to avoid delayed processing. The sample turnaround time is largely dependent on the number of samples in the queue. Normally, the turnaround time is around a few days for molecular weight determination and around one to two weeks for protein identification.
11. Charges will apply for all samples consented to be processed, regardless of expected or unexpected results.
12. Please feel free to contact the Facility for any inquiries on sample preparation, analysis, and result interpretation.
13. Please note that it is kindly requested to acknowledge the Biosciences Central Research Facility, HKUST in your publications.

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All rules and regulations will be revised regularly.